

This sequence represents an alpha-2 antiplasmin derived peptide. Alpha-2 antiplasmin is a substrate for the fibrin stabilising enzyme Factor XIIIa. Synthetic analogues of lysine and glutamine labelled with a

CC detectable moiety can also act as substrates for Factor XIIIa. The
CC invention relates to compounds which can be used in the diagnosis of
CC thrombosis or embolism and also for diagnosing atherosclerosis,
CC inflammation or cancer. The peptide forms part of the compound
XX
SQ Sequence 13 AA;
Query Match 100.0%; Score 67; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NQEQVSPYTLKKG 13
DB 1 NQEQVSPYTLKKG 13
RESULT 2
ADP44607 standard; peptide; 13 AA.
XX
AC ADP44607;
XX
DT 12-AUG-2004 (first entry)
XX
DE Radioisotope technetium-related alpha-antiplasmin mutant peptide 2.
XX
KW radioisotope technetium; Tc complex; aza-diaminedioxime ligand;
KW radiopharmaceutical; thrombus diagnostic imaging; alpha-antiplasmin;
KW mutant; mutin.
XX
OS Synthetic.
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /label= OTHER
FT /note= "OTHER = Optionally attached to N-acetyl group"
FT Modified-site 8 /label= OTHER
FT /note= "OTHER = Optionally iodo-Tyr. Substituted wild-
FT type Leu-Thr-Leu"
XX
PN WO2004037297-A1.
XX
XX
PD 06-MAY-2004.
XX
PF 24-OCT-2003; 2003WO-GB004573.
XX
PR 25-OCT-2002; 2002GB-00024799.
XX
PA (AMSH) AMERSHAM PLC.
XX
PI Brauers G, Farrar G, Barnett DJ, Wadsworth HJ, Lewis JS;
XX
DR WPI; 2004-365454/34.
XX
PT Composition useful in radiopharmaceuticals for diagnostic imaging of
PT thrombi comprises complex of radioisotope technetium with aza-
PT diaminedioxime ligand.
XX
PS Claim 9; Page 7; 50pp; English.
XX
CC The invention relates to a novel composition comprising a complex of
CC radioisotope technetium (Tc) with an aza-diaminedioxime ligand. The
CC composition of the invention may be useful in radiopharmaceuticals for
CC mammalian administration, to be used in diagnostic imaging of thrombi.
CC The composition comprises minimised amounts of lipophilic technetium.
CC complex species, thus improving the overall imaging characteristics. The
CC composition does not form a diastereomeric complex as it does not contain
CC a chiral centre and hence does not require purification of the particular
CC isomers. The current sequence is that of the radioisotope technetium (Tc)
CC -related alpha-antiplasmin mutant biological targeting peptide 2 of the
CC invention.

XX
SQ Sequence 13 AA;
Query Match 100.0%; Score 67; DB 8; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NQEQVSPYTLKKG 13
DB 1 NQEQVSPYTLKKG 13
RESULT 3
AAV67837 standard; peptide; 13 AA.
XX
AC AAV67837;
XX
DT 25-APR-2000 (first entry)
XX
DE Alpha-2 antiplasmin enzyme derived peptide #4.
XX
KW Alpha-2 antiplasmin; fibrin stabilising enzyme; Factor XIIIa; cancer;
KW embolism; thrombosis; inflammation; atherosclerosis; diagnosis.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "N-terminal acetyl"
FT
XX
PN WO9960018-A1.
XX
XX
PD 25-NOV-1999.
XX
PF 14-MAY-1999; 99WO-GB001550.
XX
PR 15-MAY-1998; 98EP-00303872.
XX
PA (AMSH) NYCOMED AMERSHAM PLC.
XX
PI Storey AE, Mendizabal M, Champion S, Gibson A, Guilbert B;
PI Wilson IA, Knox P;
XX
DR WPI; 2000-126380/11.
XX
PT Novel synthetic analogues for diagnosis of thrombosis, embolism,
PT atherosclerosis, inflammation or cancer.
XX
PS Example 2; Page 16; 46pp; English.
XX
CC This sequence represents an alpha-2 antiplasmin derived peptide. Alpha-2
CC antiplasmin is a substrate for the fibrin stabilising enzyme Factor
CC XIIIa. Synthetic analogues of lysine and glutamine labelled with a
CC detectable moiety can also act as substrates for Factor XIIIa. The
CC invention relates to compounds which can be used in the diagnosis of
CC thrombosis or embolism and also for diagnosing atherosclerosis,
CC inflammation or cancer. The peptide forms part of the compound
XX
SQ Sequence 13 AA;
Query Match 95.5%; Score 64; DB 3; Length 13;
Best Local Similarity 92.3%; Pred. No. 5.6e-05;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 NQEQVSPYTLKKG 13
DB 1 NQEQVSPYTLKKG 13
RESULT 4
AAV67836 standard; peptide; 13 AA.
XX
ID AAV67836

XX AC AAY67836;
XX DT 25-APR-2000 (first entry)
XX DE Alpha-2 antiplasmin enzyme derived peptide #3.
XX KW Alpha-2 antiplasmin; fibrin stabilising enzyme; Factor XIIIa; cancer;
XX KW embolism; thrombosis; inflammation; atherosclerosis; diagnosis.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Modified-site 1 /note= "N-terminal acetyl"
XX PN WO9960018-A1.
XX PD 25-NOV-1999.
XX PF 14-MAY-1999; 99WO-GB001550.
XX PR 15-MAY-1998; 98EP-00303872.
XX PA (AMSH) NYCOMED AMERSHAM PLC.
XX PI Storey AE, Mendizabal M, Champion S, Gibson A, Guilbert B;
XX PI Wilson IA, Knox P;
XX DR WPI; 2000-126380/11.
XX CC Novel synthetic analogues for diagnosis of thrombosis, embolism,
XX FT atherosclerosis, inflammation or cancer.
XX PS Example 2; Page 16; 46pp; English.
XX CC This sequence represents an alpha-2 antiplasmin derived peptide. Alpha-2
XX CC antiplasmin is a substrate for the fibrin stabilising enzyme Factor
XX CC XIIIa. Synthetic analogues of lysine and glutamine labelled with a
XX CC detectable moiety can also act as substrates for Factor XIIIa. The
XX CC invention relates to compounds which can be used in the diagnosis of
XX CC thrombosis or embolism and also for diagnosing atherosclerosis,
XX CC inflammation or cancer. The peptide forms part of the compound
XX SQ Sequence 13 AA;
Query Match 91.0%; Score 61; DB 3; Length 13;
Best Local Similarity 92.3%; Pred. No. 0.00021;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 NQEQVSPYTLKG 13
Db 1 NQEQVSPYTLKG 13
RESULT 5
AAY67842
ID AAY67842 standard; peptide; 13 AA.
XX AC AAY67842;
XX DT 25-APR-2000 (first entry)
XX DE Alpha-2 antiplasmin enzyme derived peptide #9.
XX KW Alpha-2 antiplasmin; fibrin stabilising enzyme; Factor XIIIa; cancer;
XX KW embolism; thrombosis; inflammation; atherosclerosis; diagnosis.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Modified-site 1 /note= "N-terminal acetyl"

FT Misc-difference 8 /note= "D-form residue"
FT Misc-difference 12 /note= "D-form residue"
FT Modified-site 13 /label= bala
XX WO9960018-A1.
XX PD 25-NOV-1999.
XX PF 14-MAY-1999; 99WO-GB001550.
XX PR 15-MAY-1998; 98EP-00303872.
XX PA (AMSH) NYCOMED AMERSHAM PLC.
XX PI Storey AE, Mendizabal M, Champion S, Gibson A, Guilbert B;
XX PI Wilson IA, Knox P;
XX DR WPI; 2000-126380/11.
XX CC Novel synthetic analogues for diagnosis of thrombosis, embolism,
XX FT atherosclerosis, inflammation or cancer.
XX PS Example 2; Page 17; 46pp; English.
XX CC This sequence represents an alpha-2 antiplasmin derived peptide. Alpha-2
XX CC antiplasmin is a substrate for the fibrin stabilising enzyme Factor
XX CC XIIIa. Synthetic analogues of lysine and glutamine labelled with a
XX CC detectable moiety can also act as substrates for Factor XIIIa. The
XX CC invention relates to compounds which can be used in the diagnosis of
XX CC thrombosis or embolism and also for diagnosing atherosclerosis,
XX CC inflammation or cancer. The peptide forms part of the compound
XX SQ Sequence 13 AA;
Query Match 91.0%; Score 61; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 NQEQVSPYTLK 12
Db 1 NQEQVSPYTLK 12
RESULT 6
AAY67841
ID AAY67841 standard; peptide; 13 AA.
XX AC AAY67841;
XX DT 25-APR-2000 (first entry)
XX DE Alpha-2 antiplasmin enzyme derived peptide #8.
XX KW Alpha-2 antiplasmin; fibrin stabilising enzyme; Factor XIIIa; cancer;
XX KW embolism; thrombosis; inflammation; atherosclerosis; diagnosis.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Modified-site 1 /note= "N-terminal acetyl"
XX FT Modified-site 8 /note= "2-Naphthylalanine"
XX PN WO9960018-A1.
XX PD 25-NOV-1999.
XX PF 14-MAY-1999; 99WO-GB001550.
XX

PR 15-MAY-1998; 98EP-00303872.
 XX (AMSH) NYCOMED AMERSHAM PLC.
 XX Storey AE, Mendizabal M, Champion S, Gibson A, Guilbert B;
 XX Wilson IA, Knox P;
 XX WPI; 2000-126380/11.
 XX Novel synthetic analogues for diagnosis of thrombosis, embolism,
 XX atherosclerosis, inflammation or cancer.
 XX Example 2; Page 16; 46pp; English.
 XX This sequence represents an alpha-2 antiplasmin derived peptide. Alpha-2
 CC antiplasmin is a substrate for the fibrin stabilising enzyme Factor
 CC XIIIa. Synthetic analogues of lysine and glutamine labelled with a
 CC detectable moiety can also act as substrates for Factor XIIIa. The
 CC detectable moiety can also act as substrates for Factor XIIIa. The
 CC invention relates to compounds which can be used in the diagnosis of
 CC thrombosis or embolism and also for diagnosing atherosclerosis,
 CC inflammation or cancer. The peptide forms part of the compound
 XX
 XX Sequence 13 AA;
 SQ

Query Match 88.1%; Score 59; DB 3; Length 13;
 Best Local Similarity 92.3%; Pred. No. 0.00049;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NQEQVSPYTLKG 13
 DB 1 NQEQVSPYTLKG 13

RESULT 7
 AAY67840
 ID AAY67840 standard; peptide; 13 AA.
 XX
 XX AAY67840;
 XX 25-APR-2000 (first entry)
 DT Alpha-2 antiplasmin enzyme derived peptide #7.
 DE Alpha-2 antiplasmin; fibrin stabilising enzyme; Factor XIIIa; cancer;
 XX embolism; thrombosis; inflammation; atherosclerosis; diagnosis.
 XX Synthetic.
 XX Key Location/Qualifiers
 XX Modified-site 1 /note= "N-terminal acetyl"
 XX W09960018-A1.
 XX 25-NOV-1999.
 XX 14-MAY-1999; 99WO-GB001550.
 XX 15-MAY-1998; 98EP-00303872.
 XX (AMSH) NYCOMED AMERSHAM PLC.
 XX Storey AE, Mendizabal M, Champion S, Gibson A, Guilbert B;
 XX Wilson IA, Knox P;
 XX WPI; 2000-126380/11.
 XX Novel synthetic analogues for diagnosis of thrombosis, embolism,
 XX atherosclerosis, inflammation or cancer.
 XX Example 2; Page 16; 46pp; English.
 XX This sequence represents an alpha-2 antiplasmin derived peptide. Alpha-2

CC antiplasmin is a substrate for the fibrin stabilising enzyme Factor
 CC XIIIa. Synthetic analogues of lysine and glutamine labelled with a
 CC detectable moiety can also act as substrates for Factor XIIIa. The
 CC invention relates to compounds which can be used in the diagnosis of
 CC thrombosis or embolism and also for diagnosing atherosclerosis,
 CC inflammation or cancer. The peptide forms part of the compound
 XX
 XX Sequence 13 AA;
 SQ

Query Match 88.1%; Score 59; DB 3; Length 13;
 Best Local Similarity 92.3%; Pred. No. 0.00049;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NQEQVSPYTLKG 13
 DB 1 NQEQVSPYTLKG 13

RESULT 8
 AAY67844
 ID AAY67844 standard; peptide; 13 AA.
 XX
 XX AAY67844;
 XX 25-APR-2000 (first entry)
 DT Alpha-2 antiplasmin enzyme derived peptide #11.
 DE Alpha-2 antiplasmin; fibrin stabilising enzyme; Factor XIIIa; cancer;
 XX embolism; thrombosis; inflammation; atherosclerosis; diagnosis.
 XX Synthetic.
 XX W09960018-A1.
 XX 25-NOV-1999.
 XX 14-MAY-1999; 99WO-GB001550.
 XX 15-MAY-1998; 98EP-00303872.
 XX (AMSH) NYCOMED AMERSHAM PLC.
 XX Storey AE, Mendizabal M, Champion S, Gibson A, Guilbert B;
 XX Wilson IA, Knox P;
 XX WPI; 2000-126380/11.
 XX Novel synthetic analogues for diagnosis of thrombosis, embolism,
 XX atherosclerosis, inflammation or cancer.
 XX Example 2; Page 17; 46pp; English.
 XX This sequence represents an alpha-2 antiplasmin derived peptide. Alpha-2
 CC antiplasmin is a substrate for the fibrin stabilising enzyme Factor
 CC XIIIa. Synthetic analogues of lysine and glutamine labelled with a
 CC detectable moiety can also act as substrates for Factor XIIIa. The
 CC invention relates to compounds which can be used in the diagnosis of
 CC thrombosis or embolism and also for diagnosing atherosclerosis,
 CC inflammation or cancer. The peptide forms part of the compound
 XX
 XX Sequence 13 AA;
 SQ

Query Match 68.7%; Score 46; DB 3; Length 13;
 Best Local Similarity 69.2%; Pred. No. 0.14;
 Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 NQEQVSPYTLKG 13
 DB 1 NQEQVSPYTLKG 13

RESULT 9
 RESULT 9

AAM50298
 ID AAM50298 standard; peptide; 13 AA.
 XX
 AC AAM50298;
 XX
 DT 04-FEB-2002 (first entry)
 XX
 DE Factor XIIIa substrate-polylysine peptide chimera.
 XX
 KW Tissue engineering; tissue repair; tissue regeneration; drug delivery;
 KW Factor XIIIa; heparin.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "dansyl leucine, allows detection of peptide by
 FT fluorescence"
 FT Peptide 2..8
 FT /note= "Factor XIIIa substrate"
 FT Peptide 9..13
 FT /note= "heparin-binding peptide"
 XX
 PN WO200183522-A2.
 XX
 FD 08-NOV-2001.
 XX
 XX 01-MAY-2000; 2000WO-US011947.
 PF
 XX 01-MAY-2000; 2000WO-US011947.
 PR
 XX (EIDG-) EIDGNOESSISCHE TECH HOCHSCHULE ZUERICH.
 PA (HUBB/) HUBBELL J A.
 PA
 XX Hubbell JA, Schense JC, Sakiyama-Elbert SE;
 PI
 XX WPT; 2002-041479/05.
 DR
 XX Novel growth factor modified protein matrix useful for tissue repair,
 PT regeneration and/or remodeling, and/or drug delivery.
 PT
 XX Example 2; Page 25; 51pp; English.
 PS
 XX The present sequence is that of a fluorescent synthetic peptide, which
 CC has a Factor XIIIa substrate at the N-terminal end and a polylysine
 CC moiety at the C-terminus. The peptide is used to produce a heparin-
 CC peptide chimera by coupling to a heparin oligosaccharide, with a unique
 CC aldehyde group on one end, via reductive amination. A matrix is formed in
 CC which heparin is used to incorporate heparin-binding growth factors for
 CC use in tissue repair, regeneration, remodeling, and/or drug delivery. The
 CC invention provides biocompatible and biodegradable matrices incorporating
 CC bioactive proteins such as growth factors. The matrices can be formed in
 CC vitro or in vivo at the site of implantation, and provide controlled
 CC and/or sustained release of the bioactive protein
 XX
 SQ Sequence 13 AA;
 Query Match 53.7%; Score 36; DB 5; Length 13;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 NOEQVSP 7
 Db 2 NOEQVSP 8
 RESULT 10
 ABG73917
 ID ABG73917 standard; peptide; 13 AA.
 XX
 AC ABG73917;
 XX
 DT 27-MAR-2003 (first entry)

XX
 DE Factor XIIIa cleavage site-containing peptide #1.
 XX
 KW Factor XIIIa; fibrin matrix; heparin; heparin binding protein; HBP;
 KW wound healing; vasculature; skin; nerve; liver.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /label= OTHER
 FT /note= "Dansyl-leucine, used to allow detection by
 FT fluorescence"
 XX
 PN US6468731-B1.
 XX
 PD 22-OCT-2002.
 XX
 PF 29-SEP-2000; 2000US-00675922.
 XX
 PR 27-AUG-1998; 98US-00141153.
 XX
 PA (EIDG-) EIDGNOESSISCHE TECH HOCHSCHULE ZUERICH.
 PA (UYZU-) UNIV ZURICH.
 XX
 PI Hubbell JA, Schense JC, Sakiyama SE;
 XX
 DR WPT; 2003-155552/15.
 XX
 XX Novel matrix for controlled delivery of heparin binding protein has
 PT fibrin, peptide having first domain with Factor XIIIa substrate and
 PT second domain with heparin/heparin-like compound, and heparin binding
 PT protein.
 XX
 PS Example 2; Col 6; 17pp; English.
 XX
 CC The invention relates to a matrix comprising fibrin, a peptide which
 CC comprises a first domain comprising a Factor XIIIa substrate and a
 CC second domain comprising heparin or a heparin-like compound coupled to
 CC the first domain, and a heparin binding protein (HBP), where the peptide
 CC is covalently attached to the fibrin through the first domain. The matrix
 CC is used for controlled release of HBP, for enhanced wound healing in
 CC various tissues including vasculature, skin, nerve and liver. Heparin
 CC used in the matrix protects the growth factors from proteolytic
 CC degradation and prolong their activity until they are released from the
 CC matrix. Despite their relatively strong affinity for heparin, heparin
 CC binding growth factors dissociate from the matrix on a short time scale.
 CC Therefore, high excess of binding sites is essential to ensure that they
 CC do not diffuse far before they bind to the matrix again. This equilibrium
 CC also allows for the binding of free growth factor to cell surface
 CC receptors that are in close proximity to the site of dissociation. This
 CC method of controlled release provides both relatively long term binding
 CC of growth factors and rapid release of growth factors to local cells. The
 CC present sequence is a peptide used to make the matrix of the invention
 XX
 SQ Sequence 13 AA;
 Query Match 53.7%; Score 36; DB 6; Length 13;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 NOEQVSP 7
 Db 2 NOEQVSP 8
 RESULT 11
 ADL46294
 ID ADL46294 standard; peptide; 13 AA.
 XX
 AC ADL46294;
 XX
 DT 20-MAY-2004 (first entry)

XX DE UDP-N-acetylglucosamine 1-carboxyvinyl transferase-1 epitope #3.
XX
XX epitope; antibacterial;
KW UDP-N-acetylglucosamine 1-carboxyvinyl transferase-1;
KW CTP:CMP-3-deoxy-D-manno-octulosonate transferase;
KW UDP-N-acetylmuramylalanyl-D-glutamate-2-6-diaminopimelate ligase;
KW D-alanine-D-alanine adding enzyme; D-alanine-D-alanine ligase;
KW UDP-N-acetylpyruvoylglycosamine reductase;
KW UDP-N-acetylglucosamine pyrophosphorylase;
KW UDP-N-acetylmuramoylalanine-D-glutamate ligase;
KW DP-N-acetylmuramate:alanine ligase; aspartate semialdehyde dehydrogenase;
KW UDP-N-acetylmuramoylalanyl-D-glutamate; X-ray diffraction analysis;
KW enzyme.
XX
XX Streptococcus pneumoniae.
OS
XX
XX WO2003087353-A2.
PN
XX
XX 23-OCT-2003.
PD
XX
XX 08-APR-2003; 2003WO-CA000481.
PF
XX
XX 08-APR-2002; 2002US-0370899P.
PR 08-APR-2002; 2002US-0370915P.
PR 09-APR-2002; 2002US-0371107P.
PR 09-APR-2002; 2002US-0371185P.
PR 31-MAY-2002; 2002US-0385426P.
PR 06-JUN-2002; 2002US-0386283P.
PR 01-AUG-2002; 2002US-0400348P.
PR 06-NOV-2002; 2002US-0424393P.
PR 08-NOV-2002; 2002US-0425200P.
PR 24-DEC-2002; 2002US-0436345P.
PR 24-DEC-2002; 2002US-0436349P.
PR 26-DEC-2002; 2002US-0436568P.
PR 27-DEC-2002; 2002US-0436673P.
PR 27-DEC-2002; 2002US-0436734P.
PR 27-DEC-2002; 2002US-0436885P.
PR 27-DEC-2002; 2002US-0436889P.
PR 27-DEC-2002; 2002US-0436893P.
PR 27-DEC-2002; 2002US-0436900P.
PR 30-DEC-2002; 2002US-0437013P.
XX
XX (AFFI-) AFFINIUM PHARM INC.
PA
XX Edwards A, Dharmsi A, Vedadi M, Domagala M, Houston S, Awrey D;
PI Beattie B, Mansoury K, Ouyang H, Vallee F, Richards D, Nethery K;
PI Virag C, Buzadzija K, Pinder B, Alam MZ, Tai M, Canadian V;
PI Kanagarajah D, Thalakada R;
XX
XX WPI; 2003-865361/80.
DR
XX
XX New recombinant bacterial enzymes involved in cell membrane biogenesis,
PT useful for designing potential antibacterial agents.
PT
XX
XX Disclosure; SEQ ID NO 12; 407pp; English.
PS
XX
XX The invention relates to isolated, recombinant polypeptides (I) that have
CC at least one activity of specified bacterial enzymes involved in cell
CC membrane biogenesis. (I) are: UDP-N-acetylglucosamine 1-carboxyvinyl
CC transferase-1 of Streptococcus pneumoniae (S.p.), Pseudomonas aeruginosa
CC (P.a.) or Staphylococcus aureus (S.a.); CTP:CMP-3-deoxy-D-manno-
CC octulosonate transferase of Escherichia coli (E.c.) or Haemophilus
CC influenzae (H.i.); UDP-N-acetylmuramylalanyl-D-glutamate-2,6-
CC diaminopimelate ligase of P.a.; D-alanine-D-alanine adding enzyme of S.a.
CC or P.a.; D-alanine-D-alanine ligase of Enterococcus faecalis (E.f.); UDP-N-
CC acetylpyruvoylglycosamine reductase of P.a. or H.i.; UDP-N-
CC acetylglucosamine pyrophosphorylase of E.f., H.i. or S.a.; UDP-N-
CC acetylmuramoylalanine-D-glutamate ligase of E.f. or H.i.; DP-N-
CC acetylmuramate:alanine ligase of E.c.; and aspartate semialdehyde
CC dehydrogenase of H.i. and UDP-N-acetylmuramoylalanyl-D-glutamate (sic) of
CC H.i. Crystalline (I) are used to determine (by X-ray diffraction
CC analysis) the structural coordinates of (I), and these then used to

CC design modulators of (I), potential therapeutic agents for treating
CC diseases caused by the specified bacteria. This sequence represents an
CC epitope from one of the proteins of the invention.
XX
XX Sequence 13 AA;
SQ
Query Match 41.8%; Score 28; DB 7; Length 13;
Best Local Similarity 62.5%; Pred. No. 3.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 5 VSPYTLK 12
DB 5 VAPYELVK 12
[::] [::]
RESULT 12
AAY20946
ID AAY20946 standard; protein; 13 AA.
XX
XX AAY20946;
AC
XX 22-JUL-1999 (first entry)
DT
XX Human presenilin II mutant protein fragment 39.
DE
XX Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;
frameshift mutation; age-related disease; neurodegenerative disorder;
KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
KW Huntington's disease; multiple sclerosis; alcoholic liver disease;
KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;
KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;
KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;
KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;
KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;
KW high mobility group protein-C; neuroendocrine specific protein A.
XX
XX Synthetic.
OS
XX Homo sapiens.
OS
XX WO9845322-A2.
PN
XX 15-OCT-1998.
XX
XX 02-APR-1998; 98WO-IB000705.
XX
XX 10-APR-1997; 97US-0043163P.
XX
XX (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.
PA (UYRO-) UNIV ROTTERDAM ERASMUS.
PA (UYUT-) RIJKSUNIV UTRECHT.
XX
XX Van Leeuwen FW, Grosveld FG, Burbach JPH;
PI
XX WPI; 1998-609901/51.
DR
XX N-PSDB; AAX75762.
XX
XX Diagnosing disease by detecting frameshift mutations in RNA or
PT corresponding protein mutations - used to diagnose cancer and
PT neurological diseases, particularly Alzheimer's disease, and also for
PT treatment and prevention with specific ribozymes or wild-type RNA.
XX
XX Disclosure; Fig 11; 258pp; English.
PS
XX This invention describes a novel method for the diagnosis of a disease
CC caused by, or associated with, an RNA molecule that has a frameshift
CC mutation. The method is used to diagnose age-related diseases, especially
CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's
CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease,
CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II
CC and many others listed) or susceptibility to these disorders. The method
CC allows a definitive diagnosis of Alzheimer's disease in living patients,
CC at an early stage. It is based on the observation that disease may be
CC caused by mutations in RNA rather than DNA. The invention describes the

CC used of neuronal system RNA molecules, specifically proteins including
 CC beta-amyloid precursor protein (beta-APP), the microtubule associated
 CC proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule
 CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,
 CC neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic
 CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma
 CC 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group
 CC protein-C (HMGP-C) and neuroendocrine specific protein A
 XX
 SQ Sequence 13 AA;
 Query Match 40.3%; Score 27; DB 2; Length 13;
 Best Local Similarity 44.4%; Pred. No. 5.4e+02;
 Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 QEQVSPYTL 10
 Db 4 RREMSPYSL 12
 RESULT 13
 ID AAY20420 standard; protein; 13 AA.
 XX
 AC AAY20420;
 XX
 DT 22-JUL-1999 (first entry)
 XX
 DE Human microtubule associated protein 2 mutant fragment 116.
 XX
 KW Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;
 KW frameshift mutation; age-related disease; neurodegenerative disorder;
 KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
 KW Huntington's disease; multiple sclerosis; alcoholic liver disease;
 KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;
 KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;
 KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;
 KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;
 KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;
 KW high mobility group protein-C; neuroendocrine specific protein A.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FN WO9845322-A2.
 XX
 PD 15-OCT-1998.
 XX
 PF 02-APR-1998; 98WO-IB000705.
 XX
 PR 10-APR-1997; 97US-0043163P.
 XX
 PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.
 PA (UYRO-) UNIV ROTTERDAM ERASMUS.
 PA (UYUT-) RIJKSUNIV UTRECHT.
 XX
 PI Van Leeuwen FW, Grosveld FG, Burbach JPH;
 XX
 XX WPI; 1998-609901/51.
 DR N-PSDB; AAX75757.
 DR
 XX
 XX Diagnosing disease by detecting frameshift mutations in RNA or
 PT corresponding protein mutations - used to diagnose cancer and
 PT neurological diseases, particularly Alzheimer's disease, and also for
 PT treatment and prevention with specific ribozymes or wild-type RNA.
 XX
 PS Disclosure; Fig 6; 258pp; English.
 XX
 XX This invention describes a novel method for the diagnosis of a disease
 CC caused by, or associated with, an RNA molecule that has a frameshift
 CC mutation. The method is used to diagnose age-related diseases, especially
 CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's
 CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease,

CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II
 CC and many others listed) or susceptibility to these disorders. The method
 CC allows a definitive diagnosis of Alzheimer's disease in living patients,
 CC at an early stage. It is based on the observation that disease may be
 CC caused by mutations in RNA rather than DNA. The invention describes the
 CC use of neuronal system RNA molecules, specifically proteins including
 CC beta-amyloid precursor protein (beta-APP), the microtubule associated
 CC proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule
 CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,
 CC neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic
 CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma
 CC 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group
 CC protein-C (HMGP-C) and neuroendocrine specific protein A
 XX
 SQ Sequence 13 AA;
 Query Match 38.8%; Score 26; DB 2; Length 13;
 Best Local Similarity 66.7%; Pred. No. 8.3e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 QEQVSP 7
 Db 3 QEEISP 8
 RESULT 14
 ID AAR54972 standard; peptide; 13 AA.
 XX
 AC AAR54972;
 XX
 DT 25-MAR-2003 (revised)
 DT 31-OCT-1994 (first entry)
 XX
 DE SorHI grass pollen allergen T cell epitope.
 XX
 KW IGE; allergy; antigen; diagnosis; treatment; Group I allergen.
 XX
 OS Sorghum halepense.
 XX
 FN WO9410314-A1.
 XX
 PD 11-MAY-1994.
 XX
 PF 29-OCT-1993; 93WO-AU000559.
 XX
 PR 30-OCT-1992; 92US-00971096.
 XX
 PA (UYME) UNIV MELBOURNE.
 XX
 PI Singh MB, Knox RB, AviJooglu A;
 XX
 XX WPI; 1994-167469/20.
 DR
 XX DNA encoding allergenic proteins and peptide(s) from Johnson grass pollen
 PT allergen SorHI - for diagnosing, treating and preventing allergy to
 PT Johnson pollen.
 XX
 PS Claim 20; Fig 9; 81pp; English.
 XX
 XX The sequence is that of a SorHI Group I grass pollen allergen T cell
 CC epitope corresp. to residues 93-105 of SorHI clone 38. See also AAR54949-
 CC 76. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 13 AA;
 Query Match 37.3%; Score 25; DB 2; Length 13;
 Best Local Similarity 50.0%; Pred. No. 1.3e+03;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 NQEQVSPY 8
 Db 4 NYEQIAAY 11

Search completed: April 12, 2005, 10:48:58
Job time : 169 secs

RESULT 15
AAW38008
ID AAW38008 standard; peptide; 13 AA.
XX AC AAW38008;
XX DT 23-APR-1998 (first entry)
XX DE WW domain binding clone 4 obtained from a pp library.
XX KW Peptide recognition unit; WW domain; cell signalling; growth regulation;
XX KW cytoskeleton organisation; targeted drug screening; modulator;
XX KW WW domain interaction.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Region 6..9
FT /note= "PPPPY motif"
XX PN W09737223-A1.
XX PD 09-OCT-1997.
XX PF 03-APR-1997; 97WO-US005547.
XX PR 03-APR-1996; 96US-00630916.
XX PA (CYTO-) CYTOGEN CORP.
XX PA (UYN-) UNIV NORTH CAROLINA.
XX PI Pirozzi G, Kay BK, Fowlkes DM;
XX WI 1997-503234/46.
XX PT Identifying cell signalling and growth regulatory polypeptides by
PT reaction with multivalent recognition complex - polypeptides are useful
PT in targeted drug selection.
XX PS Claim 92; Fig 27; 220pp; English.
XX CC Peptides AAW38005-08 are the sequences of WW domain binding clones
CC obtained by screening random or biased libraries with the WW domains of
CC the novel WWP proteins. The present peptide was obtained after screening
CC with WW domain 1 of WWP1 (WWP1.1). The peptides are peptide recognition
CC units ("ligands"), and are used for analysing specificities of the WW
CC domains. The WW domain is a small functional domain. Its name is derived
CC from the observation that two tryptophan residues, one in the amino
CC terminal portion of the WW domain and one in the carboxyl terminal
CC portion, are conserved. Most proteins containing WW domains have a
CC function involving cell signalling and growth regulation or the
CC organisation of the cytoskeleton. Polypeptides containing a WW domain are
CC identified by treating a multivalent recognition unit complex that has
CC selective binding affinity for a WW domain, with many polypeptides and
CC identifying those with selective affinity for the complex. Proteins
CC containing WW domains are used for targeted drug screening, i.e. to
CC identify potential modulators of specific WW domain interactions. note:
CC sequence in SEQ ID listing differs from sequence given in figure. The SEQ
CC ID sequence is as follows: GPSEQPPPYETVK
XX
XX Sequence 13 AA;

Query Match 37.3%; Score 25; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 3 EQVSPYTLK 12
DB 4 EQPPPYETVK 13

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OM protein - protein search, using: sw model

Run on: April 12, 2005, 10:46:01 ; Search time 40 Seconds
(without alignments)
24.261 Million cell updates/sec

Title: US-09-674-616A-2

Perfect score: 67
Sequence: 1 NQEQVSPYTLKG 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 7164

Minimum DB seq length: 13
Maximum DB seq length: 13

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA*
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	53.7	13	4	US-09-675-922-1
2	24	35.8	13	1	US-08-174-467-6
3	24	35.8	13	1	US-08-452-071-6
4	23	34.3	13	1	US-08-620-213-3
5	23	34.3	13	2	US-08-542-686-1
6	23	34.3	13	2	US-08-332-562A-69
7	22	32.8	13	1	US-08-068-947-14
8	22	32.8	13	1	US-08-068-947-15
9	22	32.8	13	3	US-08-750-419A-22
10	22	32.8	13	3	US-09-468-578-11
11	22	32.8	13	4	US-09-868-839-11
12	22	32.8	13	4	US-09-811-672-19
13	21	31.3	13	1	US-08-068-947-19
14	20.5	30.6	13	3	US-09-040-216-8
15	20	29.9	13	1	US-08-068-947-21
16	20	29.9	13	3	US-08-630-916A-6
17	20	29.9	13	3	US-08-630-916A-86
18	20	29.9	13	3	US-08-630-915A-142
19	20	29.9	13	3	US-09-297-369A-7
20	20	29.9	13	4	US-09-635-872A-52
21	20	29.9	13	4	US-09-636-077A-52
22	20	29.9	13	4	US-09-543-608A-29
23	20	29.9	13	4	US-09-543-608A-30
24	20	29.9	13	4	US-09-543-608A-31
25	20	29.9	13	4	US-09-636-060C-52
26	20	29.9	13	4	US-09-586-552-52
27	20	29.9	13	4	US-09-879-957-142

28 20 29.9 13 4 US-09-636-596C-52 Sequence 52, Appl
29 20 29.9 13 4 US-10-306-686-52 Sequence 52, Appl
30 19 28.4 13 1 US-08-068-947-8 Sequence 8, Appl
31 19 28.4 13 1 US-08-068-947-24 Sequence 24, Appl
32 19 28.4 13 1 US-08-469-005A-13 Sequence 13, Appl
33 19 28.4 13 1 US-08-188-426-7 Sequence 7, Appl
34 19 28.4 13 1 US-08-471-033-11 Sequence 11, Appl
35 19 28.4 13 2 US-08-471-044-11 Sequence 11, Appl
36 19 28.4 13 2 US-08-463-483A-11 Sequence 11, Appl
37 19 28.4 13 2 US-08-469-009-7 Sequence 7, Appl
38 19 28.4 13 2 US-08-470-566B-11 Sequence 11, Appl
39 19 28.4 13 2 US-08-470-566B-11 Sequence 11, Appl
40 19 28.4 13 2 US-08-469-007-7 Sequence 7, Appl
41 19 28.4 13 2 US-08-838-219B-11 Sequence 11, Appl
42 19 28.4 13 2 US-08-469-334-11 Sequence 11, Appl
43 19 28.4 13 3 US-08-630-916A-58 Sequence 58, Appl
44 19 28.4 13 3 US-08-881-094-42 Sequence 42, Appl
45 19 28.4 13 3 US-09-300-529-11 Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-09-675-922-1
; Sequence 1, Application US/09675922
; Patent No. 6468731
; GENERAL INFORMATION:
; APPLICANT: Hubbell A., Jeffrey
; APPLICANT: Schense C., Jason
; APPLICANT: Sakiyama E., Shelley
; TITLE OF INVENTION: Enzyme-Mediated Modification of Fibrin for Tissue
; TITLE OF INVENTION: Engineering: Incorporation of Proteins
; FILE REFERENCE: ETH 107 DIV
; CURRENT APPLICATION NUMBER: US/09/675,922
; CURRENT FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Factor XIIa at
; OTHER INFORMATION: N-terminus and modified peptide from the
; OTHER INFORMATION: heparin-binding domain of ATIII
; NAME/KEY: MOD RES
; LOCATION: (1)-
; OTHER INFORMATION: dansyl leucine
US-09-675-922-1

Query Match 53.7%; Score 36; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NQEQVSP 7
Db 2 NQEQVSP 8

RESULT 2
US-08-174-467-6
; Sequence 6, Application US/08174467
; Patent No. 5451514
; GENERAL INFORMATION:
; APPLICANT: BOUBET, ALAIN M.
; APPLICANT: INZE, DIRK G.
; APPLICANT: SCHUCH, WOLFGANG W.
; TITLE OF INVENTION: MODIFICATION OF LIGNIN SYNTHESIS IN
; TITLE OF INVENTION: PLANTS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN

STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/174,467
FILING DATE: 28-DEC-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/874,166
FILING DATE: 27-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 95563/PS36321/US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-174-467-6

Query Match 35.8%; Score 24; DB 1; Length 13;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0;

QY 5 VSPYT 9
Db 5 LSPYT 9

RESULT 3
US-08-452-071-6
Sequence 6, Application US/08452071
Patent No. 6066780
GENERAL INFORMATION:
APPLICANT: BOUDET, ALAIN M.
APPLICANT: INZE, DIRK G.
APPLICANT: SCHUCH, WOLFGANG W.
TITLE OF INVENTION: MODIFICATION OF LIGNIN SYNTHESIS IN
TITLE OF INVENTION: PLANTS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,071
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/874,166
FILING DATE: 27-APR-1992
ATTORNEY/AGENT INFORMATION:

NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 95563/PS36321/US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-452-071-6

Query Match 35.8%; Score 24; DB 3; Length 13;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0;

QY 5 VSPYT 9
Db 5 LSPYT 9

RESULT 4
US-08-620-213-3
Sequence 3, Application US/08620213
Patent No. 5677297
GENERAL INFORMATION:
APPLICANT: WALDECK, Harald
APPLICANT: HOELTJE, Dagmar
APPLICANT: MESSINGER, Josef
APPLICANT: ANTEL, Jochen
APPLICANT: WURL, Michael
APPLICANT: THORMAEHL, Dirk
TITLE OF INVENTION: BENZAZEPINE-, BENZOXAZEPINE- AND
TITLE OF INVENTION: BENZOTHIAZEPINE-N-ACETIC ACID DERIVATIVES, PROCESS FOR THEIR
TITLE OF INVENTION: PREPARATION AND PHARMACEUTICAL COMPOSITIONS CONTAINING THEM
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/620,213
FILING DATE:
CLASSIFICATION: 544
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 195 10 566.4
FILING DATE: 23-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 181/42626
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-620-213-3

Query Match 34.3%; Score 23; DB 1; Length 13;
Best Local Similarity 62.5%; Pred. No. 6e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 EQVSPYTLK 10
Db 5 EHVVPYGL 12

RESULT 5
US-08-542-686-1
; Sequence 1, Application US/08542686
; Patent No. 5824487
; GENERAL INFORMATION:
; APPLICANT: Ravetch, Jeffrey V.
; APPLICANT: Kurosaki, Tomohiro
; TITLE OF INVENTION: METHOD FOR SCREENING FOR TARGETS FOR
; TITLE OF INVENTION: ANTI-INFLAMMATORY OR ANTI-ALLERGIC AGENTS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/542.686
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/052.269
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John J.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 42113/JPW/AKC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-542-686-1

Query Match 34.3%; Score 23; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 6e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 3 EQVSPYTLK 12
Db 2 ENTITYSLK 11

RESULT 6
US-08-332-562A-69
; Sequence 69, Application US/08332562A
; Patent No. 5985599
; GENERAL INFORMATION:
; APPLICANT: MCKENZIE, Ian F.C.

; APPLICANT: HOGARTH, Mark P.
; APPLICANT: HIBBS, Margaret L.
; APPLICANT: SCOTT, Bernadette M.
; APPLICANT: BONADONNA, Lisa
; APPLICANT: HULETT, Mark D.
; TITLE OF INVENTION: PC RECEPTOR FOR IMMUNOGLOBULIN
; NUMBER OF SEQUENCES: 136
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332.562A
; FILING DATE: 31-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/896.457
; FILING DATE: 27-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 54270/119/GRHA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-332-562A-69

Query Match 34.3%; Score 23; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 6e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 3 EQVSPYTLK 12
Db 1 ENTITYSLK 10

RESULT 7
US-08-068-947-14
; Sequence 14, Application US/08068947
; Patent No. 5470753
; GENERAL INFORMATION:
; APPLICANT: Sepetov, Nikolai
; APPLICANT: Lusakova, Olga
; APPLICANT: Krchnak, Viktor
; APPLICANT: Lebl, Michal
; TITLE OF INVENTION: PEPTIDE SEQUENCING USING MASS
; TITLE OF INVENTION: SPECTROMETRY
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/068,947
FILING DATE: 19930528
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Misrock Esq., S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7156-040-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: AMINO ACID
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-068-947-14

Query Match 32.8%; Score 22; DB 1; Length 13;
Best Local Similarity 42.9%; Pred. No. 9.3e+02;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NOEQVSP 7
| : |
Db 1 NADQIQP 7

RESULT 8
US-08-068-947-15
; Sequence 15, Application US/08068947
; Patent No. 5470753
; GENERAL INFORMATION:
; APPLICANT: Sepetov, Nikolai
; APPLICANT: Lesakova, Olga
; APPLICANT: Krchnak, Viktor
; APPLICANT: Lebl, Michal
; TITLE OF INVENTION: PEPTIDE SEQUENCING USING MASS
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/068,947
; FILING DATE: 19930528
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock Esq., S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7156-040-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown

TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-068-947-15

Query Match 32.8%; Score 22; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 9.3e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 QEQVSP 7
| : |
Db 2 QDQIQP 7

RESULT 9
US-08-750-419A-22
; Sequence 22, Application US/08750419A
; Patent No. 6008340
; GENERAL INFORMATION:
; APPLICANT: BALL, TANJA
; APPLICANT: VRTALA, SUSANNE
; APPLICANT: SPERR, WOLFGANG
; APPLICANT: VALENT, PETER
; APPLICANT: SUSANI, MARKUS
; APPLICANT: KRAFT, DIETRICH
; APPLICANT: LAFFER, SILVIA
; TITLE OF INVENTION: RECOMBINANT ALLERGEN, FRAGMENTS THEREOF, VECTORS AND HOSTS
; TITLE OF INVENTION: CORRESPONDING RECOMBINANT DNA MOLECULES, DIAGNOSTIC AND THERAPEUTIC
; TITLE OF INVENTION: CONTAINING THE DNA MOLECULES, AND FRAGMENTS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/750,419A
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY JR, GERALD M
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1614-175
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-750-419A-22

Query Match 32.8%; Score 22; DB 3; Length 13;
Best Local Similarity 50.0%; Pred. No. 9.3e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 BOVSPY 8
| : |
Db 1 EPIAPY 6

RESULT 10
US-09-468-578-11

; Sequence 11, Application US/09468578
; Patent No. 6399329
; GENERAL INFORMATION:
; APPLICANT: Wang, Huaming
; APPLICANT: Bodie, Elizabeth A.
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-3
; CURRENT APPLICATION NUMBER: US/09/468,578
; CURRENT FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: US 09/220,871
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/338,723
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Stachybotrys chartarum
US-09-468-578-11

Query Match 32.8%; Score 22; DB 3; Length 13;
Best Local Similarity 80.0%; Pred. No. 9.3e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 QVSPY 8
| | | |
Db 3 QVMPEY 7

RESULT 11
US-09-868-839-11
; Sequence 11, Application US/09868839
; Patent No. 6509307
; GENERAL INFORMATION:
; APPLICANT: UNILEVER N.V. et al.
; TITLE OF INVENTION: DETERGENT COMPOSITIONS COMPRISING PHENOL OXIDIZING
; FILE REFERENCE: C7516(V)
; CURRENT APPLICATION NUMBER: US/09/868,839
; CURRENT FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: US 09/220,871
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 09/338,723
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Stachybotrys chartarum
US-09-868-839-11

Query Match 32.8%; Score 22; DB 4; Length 13;
Best Local Similarity 80.0%; Pred. No. 9.3e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 QVSPY 8
| | | |
Db 3 QVMPEY 7

RESULT 12
US-09-811-672-19
; Sequence 19, Application US/09811672
; Patent No. 6559120
; GENERAL INFORMATION:
; APPLICANT: BALL, Tanja
; APPLICANT: VRTALA, Susanne
; APPLICANT: SPERR, Wolfgang
; APPLICANT: VALENT, Peter
; APPLICANT: SUSANI, Markus
; APPLICANT: KRAFT, Dietrich

; APPLICANT: VALENTA, Rudolf
; APPLICANT: LAFFER, Sylvia
; TITLE OF INVENTION: RECOMBINANT ALLERGEN, FRAGMENTS THEREOF, CORRESPONDING RECOMBINANT
; TITLE OF INVENTION: MOLECULES, VECTORS AND HOSTS CONTAINING THE DNA MOLECULES, DIAGN
; TITLE OF INVENTION: THERAPEUTIC USES OF SAID ALLERGENS AND FRAGMENTS
; FILE REFERENCE: 1614-0247P
; CURRENT APPLICATION NUMBER: US/09/811,672
; CURRENT FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Timothy Grass
US-09-811-672-19

Query Match 32.8%; Score 22; DB 4; Length 13;
Best Local Similarity 50.0%; Pred. No. 9.3e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 EQVSPY 8
| | | |
Db 1.EPIAPY 6

RESULT 13
US-08-068-947-19
; Sequence 19, Application US/08068947
; Patent No. 5470753
; GENERAL INFORMATION:
; APPLICANT: Sepetov, Nikolai
; APPLICANT: Lssakova, Olga
; APPLICANT: Krchnak, Viktor
; APPLICANT: Lebl, Michal
; TITLE OF INVENTION: PEPTIDE SEQUENCING USING MASS
; TITLE OF INVENTION: SPECTROMETRY
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/068,947
; FILING DATE: 19930528
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock Esq., S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7156-040-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-068-947-19

Query Match 31.3%; Score 21; DB 1; Length 13;
Best Local Similarity 42.9%; Pred. No. 1.5e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Qy 1 NQEQVSP 7
Db 1 NEQIQP 7

RESULT 14
US-09-040-216-8
; Sequence 8, Application US/09040216
; Patent No. 6030942
; GENERAL INFORMATION:
; APPLICANT: COOPERMAN, ET AL., BARRY
; TITLE OF INVENTION: PEPTIDES, PEPTIDE ANALOGS, PEPTIDOMIMETICS, AND OTHER
; TITLE OF INVENTION: SMALL MOLECULES USEFUL FOR INHIBITING THE ACTIVITY OF
; TITLE OF INVENTION: RIBONUCLEOTIDE REDUCTASE
; FILE REFERENCE: 9596-63U1
; CURRENT APPLICATION NUMBER: US/09/040.216
; CURRENT FILING DATE: 1998-03-17
; EARLIER APPLICATION NUMBER: 08/919,748
; EARLIER FILING DATE: 1997-08-28
; EARLIER APPLICATION NUMBER: 60/025,146
; EARLIER FILING DATE: 1996-08-30
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Escherichia coli
; FEATURE:
; OTHER INFORMATION: alpha 13 helix region of E. coli R1
US-09-040-216-8

Query Match 30.6%; Score 20.5; DB 3; Length 13;
Best Local Similarity 85.7%; Pred. No. 1.8e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 8 YT-LKLG 13
Db 5 YTRLKLG 11

RESULT 15
US-08-068-947-21
; Sequence 21, Application US/08068947
; Patent No. 5470753
; GENERAL INFORMATION:
; APPLICANT: Sepetov, Nikolai
; APPLICANT: Lssakova, Olga
; APPLICANT: Krchnak, Viktor
; APPLICANT: Lebl, Michal
; TITLE OF INVENTION: PEPTIDE SEQUENCING USING MASS
; TITLE OF INVENTION: SPECTROMETRY
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESS: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/068,947
; FILING DATE: 19930528
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Masrock Esq., S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7156-040-999

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-068-947-21

Query Match 29.9%; Score 20; DB 1; Length 13;
Best Local Similarity 60.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 QVSPY 8
Db 9 QVTFF 13

Search completed: April 12, 2005, 10:49:44
Job time : 41 secs
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OM protein - protein search, using sw model

Run on: April 12, 2005, 10:49:51 ; Search time 129 Seconds

(without alignments)

33.457 Million cell updates/sec

Title: US-09-674-616A-2

Perfect score: 67

Sequence: 1 NQEQVSPYLLKG 13

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1418010 seqs, 33197259 residues

Total number of hits satisfying chosen parameters: 13198

Minimum DB seq length: 13

Maximum DB seq length: 13

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

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- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
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- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	36	53.7	13	14	US-10-323-046-22	Sequence 22, Appl
2	24	35.8	13	10	US-09-932-613-156	Sequence 156, App
3	24	35.8	13	10	US-09-932-322-156	Sequence 156, App
4	24	35.8	13	15	US-10-361-208-64	Sequence 64, Appl
5	24	35.8	13	15	US-10-361-208-197	Sequence 197, App
6	24	35.8	13	17	US-10-851-637-87	Sequence 87, Appl
7	24	35.8	13	17	US-10-851-637-88	Sequence 88, Appl
8	23	34.3	13	14	US-10-226-007-782	Sequence 782, App
9	23	34.3	13	14	US-10-226-007-794	Sequence 794, App
10	23	34.3	13	14	US-10-226-007-805	Sequence 805, App
11	23	34.3	13	14	US-10-226-007-815	Sequence 815, App
12	23	34.3	13	14	US-10-226-007-824	Sequence 824, App
13	23	34.3	13	14	US-10-226-007-832	Sequence 832, App

14	23	34.3	13	15	US-10-412-897-20	Sequence 20, Appl
15	22	32.8	13	9	US-09-338-723A-7	Sequence 7, Appl
16	22	32.8	13	9	US-09-811-672-19	Sequence 19, Appl
17	22	32.8	13	9	US-09-946-175-8	Sequence 8, Appl
18	22	32.8	13	9	US-09-791-378-594	Sequence 594, App
19	22	32.8	13	10	US-09-791-393-156	Sequence 156, App
20	22	32.8	13	10	US-09-791-389-156	Sequence 156, App
21	22	32.8	13	11	US-09-791-377-594	Sequence 594, App
22	22	32.8	13	13	US-10-080-210-11	Sequence 11, Appl
23	22	32.8	13	14	US-10-153-244-78	Sequence 78, Appl
24	22	32.8	13	14	US-10-153-244-141	Sequence 141, App
25	22	32.8	13	14	US-10-153-244-191	Sequence 191, App
26	22	32.8	13	14	US-10-153-244-241	Sequence 241, App
27	22	32.8	13	14	US-10-161-860-22	Sequence 22, Appl
28	22	32.8	13	15	US-10-285-394-162	Sequence 162, App
29	22	32.8	13	16	US-10-311-509-19	Sequence 19, Appl
30	21	31.3	13	10	US-09-993-180-13	Sequence 13, Appl
31	21	31.3	13	14	US-10-104-943-12	Sequence 12, Appl
32	21	31.3	13	14	US-10-104-943-57	Sequence 57, Appl
33	21	31.3	13	14	US-10-226-007-1016	Sequence 1016, Ap
34	21	31.3	13	14	US-10-226-007-1029	Sequence 1029, Ap
35	21	31.3	13	14	US-10-226-007-1042	Sequence 1042, Ap
36	21	31.3	13	14	US-10-226-007-1055	Sequence 1055, Ap
37	21	31.3	13	14	US-10-226-007-1068	Sequence 1068, Ap
38	21	31.3	13	14	US-10-024-197-23	Sequence 23, Appl
39	21	31.3	13	14	US-10-224-999A-1786	Sequence 1786, Ap
40	21	31.3	13	14	US-10-224-999A-1787	Sequence 1787, Ap
41	21	31.3	13	14	US-10-224-999A-1788	Sequence 1788, Ap
42	21	31.3	13	14	US-10-224-999A-1789	Sequence 1789, Ap
43	21	31.3	13	14	US-10-224-999A-1790	Sequence 1790, Ap
44	21	31.3	13	15	US-10-298-461-14	Sequence 14, Appl
45	21	31.3	13	15	US-10-285-394-129	Sequence 129, App

ALIGNMENTS

RESULT 1
US-10-323-046-22
; Sequence 22, Application US/10323046
; Publication No. US20030187232A1
; GENERAL INFORMATION:
; APPLICANT: Hubbell, Jeffrey A
; APPLICANT: Schense, Jason C
; APPLICANT: Sakiyama-Elbert, Shelly E
; TITLE OF INVENTION: Growth Factor Modified Protein Matrices for Tissue
; TITLE OF INVENTION: Engineering
; FILE REFERENCE: ETH 107 CIP (2)
; CURRENT APPLICATION NUMBER: US/10323,046
; CURRENT FILING DATE: 2002-12-17
; PRIOR FILING DATE: 1998-08-27
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 22
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: dansyl Leucine
US-10-323-046-22

Query Match 53.7%; Score 36; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NQEQVSP 7

Db 2 NQEQVSP 8

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RESULT 2
US-09-932-613-156
; Sequence 156, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: Dlx-025.1 PCT: Dlx-025.1 US
; CURRENT FILING DATE: 2001-08-17
; CURRENT APPLICATION NUMBER: US/09/932,613
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 156
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-156
Query Match 35.8%; Score 24; DB 10; Length 13;
Best Local Similarity 66.7%; Pred. No. 1.5e+03;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 QVSPYTLK 12
| | | | |
Db 2 QVDPETGLK 10

RESULT 3
US-09-932-322-156
; Sequence 156, Application US/09932322
; Publication No. US20030194743A1
; GENERAL INFORMATION:
; APPLICANT: Dyax Corp.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Ladner, Robert Charles
; TITLE OF INVENTION: BINDING POLYPEPTIDES FOR B LYMPHOCYTE STIMULATOR PROTEIN (Blys)
; FILE REFERENCE: Dlx-018.1 PCT: Dlx-018.1 US
; CURRENT FILING DATE: 2001-08-17
; CURRENT APPLICATION NUMBER: US/09/932,322
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 156
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-322-156
Query Match 35.8%; Score 24; DB 10; Length 13;
Best Local Similarity 66.7%; Pred. No. 1.5e+03;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 QVSPYTLK 12
| | | | |
Db 2 QVDPETGLK 10

RESULT 4
US-10-361-208-64
; Sequence 64, Application US/10361208
; Publication No. US20040009167A1
; GENERAL INFORMATION:
; APPLICANT: Rider, Todd H.
; TITLE OF INVENTION: ANTI-PATHOGEN TREATMENTS
; FILE REFERENCE: 0050.2041-003
; CURRENT FILING DATE: 2003-02-07
; CURRENT APPLICATION NUMBER: US 60/355,359
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: US 60/355,022
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: US 60/432,386
; NUMBER OF SEQ ID NOS: 473
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 13
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: partial Hdj-1 sequence
; NAME/KEY: NON CONS
; LOCATION: 7-8
US-10-361-208-197
Query Match 35.8%; Score 24; DB 15; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QEQVSP 7
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Db 7 QEQVLP 12

RESULT 5
US-10-361-208-197
; Sequence 197, Application US/10361208
; Publication No. US20040009167A1
; GENERAL INFORMATION:
; APPLICANT: Rider, Todd H.
; TITLE OF INVENTION: ANTI-PATHOGEN TREATMENTS
; FILE REFERENCE: 0050.2041-003
; CURRENT FILING DATE: 2003-02-07
; CURRENT APPLICATION NUMBER: US/10/361,208
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: US 60/355,359
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: US 60/355,022
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: US 60/432,386
; NUMBER OF SEQ ID NOS: 473
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 197
; LENGTH: 13
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: partial Hdj-1 sequence
; NAME/KEY: NON CONS
; LOCATION: 7-8
US-10-361-208-197
Query Match 35.8%; Score 24; DB 15; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QEQVSP 7
| | | | |
Db 7 QEQVLP 12

RESULT 6
US-10-851-637-87
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; Sequence 87, Application US/10851637
; Publication No. US20050015039A1
; GENERAL INFORMATION:
; APPLICANT: Salzwedel, Karl
; APPLICANT: Li, Feng
; APPLICANT: Wild, Carl T.
; APPLICANT: Allaway, Graham P.
; APPLICANT: Freed, Eric O.
; TITLE OF INVENTION: Inhibition of HIV-1 Replication by Distribution of the Processing
; FILE REFERENCE: 1900.0430003
; CURRENT APPLICATION NUMBER: US/10/851,637
; CURRENT FILING DATE: 2004-05-24
; PRIOR FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: US 10/766,528
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US 60/496,660
; PRIOR FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: US 60/443,180
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 87
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Mutant SPI region in HIV-1 NL4-3
US-10-851-637-87

Query Match          35.8%; Score 24; DB 17; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 4 QVSPYTL 11
Db 6 QVNPATIM 13

RESULT 7
US-10-851-637-88
; Sequence 88, Application US/10851637
; Publication No. US20050015039A1
; GENERAL INFORMATION:
; APPLICANT: Salzwedel, Karl
; APPLICANT: Li, Feng
; APPLICANT: Wild, Carl T.
; APPLICANT: Allaway, Graham P.
; APPLICANT: Freed, Eric O.
; TITLE OF INVENTION: Inhibition of HIV-1 Replication by Distribution of the Processing
; FILE REFERENCE: 1900.0430003
; CURRENT APPLICATION NUMBER: US/10/851,637
; CURRENT FILING DATE: 2004-05-24
; PRIOR FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: US 10/766,528
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US 60/496,660
; PRIOR FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: US 60/443,180
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 88
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Mutant SPI region in HIV-1 NL4-3
US-10-851-637-88

Query Match          35.8%; Score 24; DB 17; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 4 QVSPYTL 11
Db 6 QVNPATIM 13
```

```
Qy 4 QVSPYTL 11
Db 6 QVNPATIM 13

RESULT 8
US-10-226-007-782
; Sequence 782, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/313,883
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 782
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Human herpesvirus 4
US-10-226-007-782

Query Match          34.3%; Score 23; DB 14; Length 13;
Best Local Similarity 50.0%; Pred. No. 2.2e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 NQEQVSPY 8
Db 1 NEEPPPPY 8

RESULT 9
US-10-226-007-794
; Sequence 794, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/313,883
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 794
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Human herpesvirus 4
US-10-226-007-794

Query Match          34.3%; Score 23; DB 14; Length 13;
Best Local Similarity 50.0%; Pred. No. 2.2e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 NQEQVSPY 8
Db 2 NEEPPPPY 9

RESULT 10
US-10-226-007-805
; Sequence 805, Application US/10226007
; Publication No. US20030105277A1
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GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 805
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Human herpesvirus 4
US-10-226-007-805

Query Match 34.3%; Score 23; DB 14; Length 13;
Best Local Similarity 50.0%; Pred. No. 2.2e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 NOEQVSPY 8
|:|:|
Db 3 NEPPPPY 10

RESULT 11
US-10-226-007-815
; Sequence 815, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 815
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Human herpesvirus 4
US-10-226-007-815

Query Match 34.3%; Score 23; DB 14; Length 13;
Best Local Similarity 50.0%; Pred. No. 2.2e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 NOEQVSPY 8
|:|:|
Db 4 NEPPPPY 11

RESULT 12
US-10-226-007-824
; Sequence 824, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15

; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 824
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Human herpesvirus 4
US-10-226-007-824

Query Match 34.3%; Score 23; DB 14; Length 13;
Best Local Similarity 50.0%; Pred. No. 2.2e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 NOEQVSPY 8
|:|:|
Db 5 NEPPPPY 12

RESULT 13
US-10-226-007-832
; Sequence 832, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 832
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Human herpesvirus 4
US-10-226-007-832

Query Match 34.3%; Score 23; DB 14; Length 13;
Best Local Similarity 50.0%; Pred. No. 2.2e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 NOEQVSPY 8
|:|:|
Db 6 NEPPPPY 13

RESULT 14
US-10-412-897-20
; Sequence 20, Application US/10412897
; Publication No. US20030220224A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES ENCODING THE HUMAN CITRON KINASE
; FILE REFERENCE: D0193 NP
; CURRENT APPLICATION NUMBER: US/10/412,897
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: U.S. 60/372,745
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-412-897-20

Query Match 34.3%; Score 23; DB 15; Length 13;

Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QEQVS 6
|
|
|
|
Db 2 QEQVS 6

RESULT 15

US-09-338-723A-7
; Sequence 7, Application US/09338723A
; Patent No. US20020019038A1
; GENERAL INFORMATION:
; APPLICANT: Huaming, Wang
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-2
; CURRENT APPLICATION NUMBER: US/09/338,723A
; CURRENT FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 09/220,871
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Stachybotrys chartarum
US-09-338-723A-7

Query Match 32.8%; Score 22; DB 9; Length 13;
Best Local Similarity 80.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 QVSPY 8
|
|
|
|
Db 3 QVMPY 7

Search completed: April 12, 2005, 11:04:24
Job time : 130 secs

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OM protein - protein search, using sw model

Run on: April 12, 2005, 10:46:01 ; Search time 42 Seconds
(without alignments)
29.781 Million cell updates/sec

Title: US-09-674-616A-2

Perfect score: 67

Sequence: 1 NOEQVSPYLLKG 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 246

Minimum DB seq length: 13

Maximum DB seq length: 13

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	29.9	13	2 S47361	T-cell antigen rec
2	20	29.9	13	2 B56864	dipeptidyl-peptida
3	19	28.4	13	2 PL0157	Ig kappa chain V-I
4	19	28.4	13	2 S32473	lynnadPamide 3 - g
5	18	26.9	13	2 B61458	Ig kappa chain V-I
6	18	26.9	13	2 A61458	Ig kappa chain V-I
7	17	25.4	13	1 UNBO	neurotensin - bovi
8	17	25.4	13	2 A44818	extracellular lipa
9	17	25.4	13	2 A28505	neurotensin [valid
10	17	25.4	13	2 A61067	neurotensin - comm
11	17	25.4	13	2 A53608	neurotensin - guin
12	17	25.4	13	2 PT0256	Ig heavy chain CRD
13	17	25.4	13	2 A05174	tryptophyllin-13 -
14	16	23.9	13	2 PC1149	equinacoxin 1A - s
15	16	23.9	13	2 A61514	glutathione transf
16	15	22.4	13	2 S15755	actin 7 - soybean
17	15	22.4	13	2 B26093	microbial collagen
18	15	22.4	13	2 A54326	glutathione transf
19	15	22.4	13	2 B28810	glutathione transf
20	15	22.4	13	2 S47358	T-cell antigen rec
21	15	22.4	13	2 PH1599	Ig H chain V-D-J r
22	14	20.9	13	2 PU0038	alpha-peptide/algi
23	14	20.9	13	2 D61458	Ig kappa chain V-I
24	14	20.9	13	2 E61458	Ig kappa chain V-I
25	14	20.9	13	2 S47362	T-cell antigen rec
26	14	20.9	13	2 S47380	T-cell antigen rec
27	14	20.9	13	2 B61233	conceptus protein
28	14	20.9	13	2 PH1595	Ig H chain V-D-J r
29	14	20.9	13	2 PH0786	T-cell receptor al

30	14	20.9	13	2 IS1905	collecting duct wa
31	14	20.9	13	2 S36668	hypothetical prote
32	14	20.9	13	2 S32471	lynnadPamide 1 - g
33	14	20.9	13	2 S32472	lynnadPamide 2 - g
34	14	20.9	13	2 A61361	bradykinin-like pe
35	13	19.4	13	2 S39413	tubulin beta chain
36	13	19.4	13	2 S36887	ribosomal protein
37	13	19.4	13	2 PH0138	T-cell receptor be
38	13	19.4	13	2 B47415	mannose-1-phosphat
39	13	19.4	13	2 G37266	Ig heavy chain C r
40	13	19.4	13	2 D37267	Ig heavy chain C r
41	13	19.4	13	2 C47630	Ig kappa chain J r
42	13	19.4	13	2 A59491	epithelial dog all
43	13	19.4	13	2 A32453	phloroglucinol red
44	13	19.4	13	2 G83988	hypothetical prote
45	13	19.4	13	2 H85575	hypothetical prote

ALIGNMENTS

RESULT 1

S47361

T-cell antigen receptor VJ junction beta chain - human

C:Species: Homo sapiens (man)

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999

C:Accession: S47361

R:Lehner, P.J.

submitted to the EMBL Data Library, August 1994

A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T ce

A:Reference number: S47355

A:Accession: S47361

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-13 <LEH>

A:Cross-references: EMBL:Z35685; NID:G527459; PIDN:CAA04754.1; PID:G527460

C:Keywords: T-cell receptor

Query Match 29.9%; Score 20; DB 2; Length 13;

Best Local Similarity 80.0%; Pred. No. 1.6e+03;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 QVSPY 8

DB 5 QGSPY 9

RESULT 2

B56864

dipeptidyl-peptidase IV (EC 3.4.14.5) - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C>Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 05-Jan-1996

C:Accession: B56864

R:Plakidou-Dymock, S.; McGivan, J.D.

Biochim. Biophys. Acta 1145, 105-112, 1993

A:Title: The oligomeric structure of renal aminopeptidase N from bovine brush-border mem

A:Reference number: A56864; MUID:93136203; PMID:8093665

A:Accession: B56864

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-13 <PLA>

A:Experimental source: renal brush-border membrane vesicles

C:Keywords: dipeptidylpeptidase hydrolase

Query Match 29.9%; Score 20; DB 2; Length 13;

Best Local Similarity 37.5%; Pred. No. 1.6e+03;

Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 SPYTLKKG 13

DB 3 TPWKVLGS 10

```

RESULT 3
PL0157
Ig kappa chain V-II region (anti-myeelin-associated glycoprotein, PEC) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-Feb-1997
C:Accession: PL0157; C61458
R:Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.
J. Exp. Med. 170, 1551-1558, 1989
A:Title: Expression of a public idiootype by human monoclonal IGM directed to myelin-assoc
A:Reference number: A61458; MUID:90039128; PMID:2478651
A:Accession: PL0157
A:Molecule type: protein
A:Residues: 1-13 <BRO>
A:Accession: C61458
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-13 <BR2>
C:Comment: This protein is one of monoclonal IGM reactive with myelin-associated glycopr
C:Keywords: glycoprotein; heterotetramer; immunoglobulin

Query Match      28.4%; Score 19; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 2.5e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 SPYTL 10
      |||
Db      7 SPVTL 11

RESULT 4
S32473
LymnaeaDFamide 3 - great pond snail
C:Species: Lymnaea stagnalis (Great pond snail)
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S32473
R:Johnsen, A.H.; Rehfeld, J.F.
Eur. J. Biochem. 213, 875-879, 1993
A:Title: LymnaeDFamides, a new family of neuropeptides from the pond snail, Lymnaea stagn
A:Reference number: S32471; MUID:93238777; PMID:8477756
A:Accession: S32473
A:Molecule type: protein
A:Residues: 1-13 <JOH>
A:Cross-references: UNIPROT:P80180; PIN: AAB26364.1; PID:G299831
A:Experimental source: ganglia
C:Keywords: amidated carboxyl end; neuropeptide
F:13/Modified site: amidated carboxyl end (phe) #status predicted

Query Match      28.4%; Score 19; DB 2; Length 13;
Best Local Similarity 42.9%; Pred. No. 2.5e+03;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      7 PYTLKG 13
      |||
Db      1 PYDRISG 7

RESULT 5
B61458
Ig kappa chain V-I region (BLA) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 16-Aug-1996
C:Accession: B61458
R:Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.
J. Exp. Med. 170, 1551-1558, 1989
A:Title: Expression of a public idiootype by human monoclonal IGM directed to myelin-assoc
A:Reference number: A61458; MUID:90039128; PMID:2478651
A:Accession: B61458
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-13 <BRO>
C:Keywords: heterotetramer; immunoglobulin

Query Match      26.9%; Score 18; DB 2; Length 13;

```

```

Best Local Similarity 80.0%; Pred. No. 3.9e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 SPYTL 10
      |||
Db      7 SPVTL 11

RESULT 6
A61458
Ig kappa chain V-I region (BOU) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 16-Aug-1996
C:Accession: A61458; PL0156
R:Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.
J. Exp. Med. 170, 1551-1558, 1989
A:Title: Expression of a public idiootype by human monoclonal IGM directed to myelin-assoc
A:Reference number: A61458; MUID:90039128; PMID:2478651
A:Accession: A61458
A:Molecule type: protein
A:Residues: 1-13 <BRO>
C:Comment: This protein is one of monoclonal IGM reactive with myeloma-associated glycopr
C:Keywords: heterotetramer; immunoglobulin

Query Match      26.9%; Score 18; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 3.9e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 SPYTL 10
      |||
Db      7 SPVTL 11

RESULT 7
UNBO
neurotensin - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 18-Dec-1981 #sequence_revision 18-Dec-1981 #text_change 24-Feb-1995
C:Accession: A01420
R:Caraway, R.; Leeman, S.E.
J. Biol. Chem. 250, 1907-1911, 1975
A:Title: The amino acid sequence of a hypothalamic peptide, neurotensin.
A:Reference number: A92172; MUID:75095678; PMID:1167549
A:Accession: A01420
A:Molecule type: protein
A:Residues: 1-13 <CAR>
R:Caraway, R.; Leeman, S.E.
J. Biol. Chem. 250, 1912-1918, 1975
A:Title: The synthesis of neurotensin.
A:Reference number: A92173; MUID:75095679; PMID:1112838
A:Contents: annotation; synthesis
A>Note: a tridecapeptide chemically and pharmacologically identical with the natural pep
C:Superfamily: neurotensin
C:Keywords: neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match      25.4%; Score 17; DB 1; Length 13;
Best Local Similarity 75.0%; Pred. No. 6e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      7 PYTL 10
      |||
Db      10 PYIL 13

RESULT 8
A44818
extracellular lipase - Pseudomonas aeruginosa (fragment)
C:Species: Pseudomonas aeruginosa
C>Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A44818
R:Gilbert, E.J.; Cornish, A.; Jones, C.W.

```

J. Gen. Microbiol. 137, 2223-2229, 1991
A;Title: Purification and properties of extracellular lipase from *Pseudomonas aeruginosa*
A;Reference number: A44818; MUID:92085040; PMID:1748875
A;Accession: A44818
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-13 <GIL>
A;Cross-references: UNIPROT:Q9L6C7; UNIPROT:P95419
A;Experimental source: strain TP3285
A;Note: sequence extracted from NCBI backbone (NCBIP:70395)
C;Superfamily: *Pseudomonas* triacylglycerol lipase

Query Match 25.4%; Score 17; DB 2; Length 13;
Best Local Similarity 57.1%; Pred. No. 6e+03; 3; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 SPYTLK 12
| | |
Db 1 STYQTQK 7

RESULT 9
A28505
neurotensin [validated] - chicken
C;Species: *Gallus gallus* (Chicken)
C;Date: 19-Nov-1988 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C;Accession: A28505
Jpn. J. Pharmacol. 44, 455-459, 1987
A;Title: The amino acid sequence of a smooth muscle-contracting peptide from chicken red
A;Reference number: A28505; MUID:88063566; PMID:3682409
A;Accession: A28505
A;Molecule type: protein
A;Residues: 1-13 <IWA>
A;Cross-references: UNIPROT:P13724
A;Experimental source: rectum
C;Comment: The peptide isolated from rectum is identical with chicken neurotensin and ha
C;Superfamily: neurotensin
C;Keywords: hormone; neurotensin; pyroglutamic acid
F;1/Modified site: neurotensin #status experimental

Query Match 25.4%; Score 17; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 6e+03; 1; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 PYTL 10
| | |
Db 10 PYIL 13

RESULT 10
A61067
neurotensin - common frog
C;Species: *Rana temporaria* (common frog)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A61067
R;Shaw, C.; McKay, D.M.; Halton, D.W.; Thim, L.; Buchanan, K.D.
Regul. Pept. 38, 23-31, 1992
A;Title: Isolation and primary structure of an amphibian neurotensin.
A;Reference number: A61067; MUID:92245104; PMID:1574601
A;Accession: A61067
A;Molecule type: protein
A;Residues: 1-13 <SHA>
A;Cross-references: UNIPROT:P41536
A;Note: this peptide was identified in brain, intestine, and rectum, but not in stomach
C;Superfamily: neurotensin
C;Keywords: brain; intestine; neurotensin; pyroglutamic acid
F;1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental

Query Match 25.4%; Score 17; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 6e+03; 1; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 PYTL 10
| | |
Db 10 PYIL 13

RESULT 11
A53608
neurotensin - guinea pig
C;Species: *Cavia porcellus* (guinea pig)
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C;Accession: A53608
R;Shaw, C.; Thim, L.; Conlon, J.M.
FEBS Lett. 202, 187-191, 1986
A;Title: [Ser(7)]neurotensin: isolation from guinea pig intestine.
A;Reference number: A53608; MUID:86248085; PMID:3087775
A;Accession: A53608
A;Molecule type: protein
A;Residues: 1-13 <SHA>
A;Cross-references: UNIPROT:P32560
C;Superfamily: neurotensin
C;Keywords: neurotensin; pyroglutamic acid
F;1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental

Query Match 25.4%; Score 17; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 6e+03; 1; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 PYTL 10
| | |
Db 10 PYIL 13

RESULT 12
PT0256
Ig heavy chain CRD3 region (clone 2-115C) - human (fragment)
C;Species: *Homo sapiens* (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0256
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0256
A;Molecule type: DNA
A;Residues: 1-13 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 25.4%; Score 17; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 6e+03; 1; Mismatches 2; Indels 0; Gaps 0;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 8 YTLKG 13
| | |
Db 4 YDLTG 9

RESULT 13
A05174
tryptophyllin-13 - Rohde's leaf frog
C;Species: *Phyllomedusa rohdei* (Rohde's leaf frog)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
C;Accession: A05174
R;Montecucchi, P.C.; Gozzini, L.; Erspamer, V.
Int. J. Pept. Protein Res. 27, 175-182, 1986
A;Reference number: A05174
A;Accession: A05174
A;Molecule type: protein
A;Residues: 1-13 <MON>
A;Cross-references: UNIPROT:P04096
C;Superfamily: unassigned animal peptides

C;Keywords: pyroglutamic acid; skin
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 25.4%; Score 17; DB 2; Length 13;
Best Local Similarity 60.0%; Pred. No. 6e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 QVSPY 8
| | | |
Db 1 QEKPY 5

RESULT 14

PC1149
equinotoxin 1A - sea anemone (Actinia equina) (fragment)
C;Species: Actinia equina.
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PC1149
R;Komatsu, S.; Furukawa, K.; Abe, K.; Hirano, H.; Ueda, M.
Chem. Pharm. Bull. 40, 2873-2875, 1992
A;Title: Isolation and characterization of equinotoxins from the sea anemone Actinia equina
A;Reference number: PC1149; MUID:93099631; PMID:1361161
A;Accession: PC1149
A;Molecule type: protein
A;Residues: 1-13 <KOM>
C;Keywords: toxin

Query Match 23.9%; Score 16; DB 2; Length 13;
Best Local Similarity 60.0%; Pred. No. 9.3e+03; Indels 0; Gaps 0;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NOEQV 5
| | | |
Db 4 NQAEV 8

RESULT 15

A61514
glutathione transferase (EC 2.5.1.18), 26k - fluke (Schistosoma japonicum) (fragment)
C;Species: Schistosoma japonicum
C;Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 09-Jul-2004
C;Accession: A61514
R;Mitchell, G.F.
Mol. Biochem. Parasitol. 27, 249-256, 1988
A;Title: Expression of an enzymatically active parasite molecule in Escherichia coli: Schistosoma japonicum glutathione transferase
A;Reference number: A61514; MUID:88142394; PMID:3278228
A;Accession: A61514
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-13 <MIT>
A;Cross-references: UNIPROT:P08515
C;Keywords: transferase

Query Match 23.9%; Score 16; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 9.3e+03; Indels 0; Gaps 0;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 8 YTLKG 13
| | | |
Db 6 YWKKG 11

Search completed: April 12, 2005, 10:50:32
Job time : 43 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 12, 2005, 10:46:02 ; Search time 174 Seconds
(without alignments)
38.259 Million cell updates/sec

Title: US-09-674-616A-2

Perfect score: 67

Sequence: 1 NQEQSPYTLKG 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 722

Minimum DB seq length: 13

Maximum DB seq length: 13

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	22	32.8	13	2	Q9UEE2	Q9uee2 homo sapien
2	20	29.9	13	1	IDHA_CANFA	P54836 canis famil
3	20	29.9	13	2	Q6T675	Q6t675 papio anubi
4	19	28.4	13	1	CHEP_PARID	P42718 parapolylbia
5	19	28.4	13	1	NP3_LYMT	P80180 lymnaea ata
6	19	28.4	13	2	Q14890	Q14890 homo sapien
7	19	28.4	13	2	Q51605	Q51605 plasmid col
8	19	28.4	13	2	Q9RG00	Q9rg00 mycoplasma
9	18	26.9	13	1	FR12_PEA	P81796 bufo marinu
10	17	25.4	13	1	NEUT_BUFMA	P83445 pisum sativ
11	17	25.4	13	1	NEUT_CAVPO	P32560 cavia porce
12	17	25.4	13	1	NEUT_CHICK	P13724 gallus gall
13	17	25.4	13	1	NEUT_RANTE	P41536 rana tempor
14	17	25.4	13	1	TY13_PHYRO	P04096 phyllomedus
15	17	25.4	13	2	Q6S4R5	Q6s4r5 leishmania
16	17	25.4	13	2	Q50476	Q50476 mycobacteri
17	16	23.9	13	1	PEDI_HVDAT	P80578 hydra atten
18	16	23.9	13	1	PROX_ORYSA	P83647 oryza sativ
19	16	23.9	13	1	SAZA_ONCMY	P82238 oncorhynch
20	16	23.9	13	1	SA23B_ONCMY	P82239 oncorhynch
21	16	23.9	13	2	Q93824	Q93824 candida tro
22	16	23.9	13	2	Q9FS94	Q9fs94 silene pent
23	16	23.9	13	2	Q9FSA8	Q9fsa8 silene bacc
24	16	23.9	13	2	Q9S8N1	Q9s8n1 hordeum vul
25	15	22.4	13	1	ACT7_SOYBN	P15987 glycine max
26	15	22.4	13	1	EI21_LITRU	P82097 litoria rub
27	15	22.4	13	1	EI22_GLOPA	P82098 litoria rub
28	15	22.4	13	1	UN12_CLOTR	P81353 clostridium
29	15	22.4	13	1	UN12_CLOTR	P82036 uperoleia i
30	15	22.4	13	2	Q47693	Q47693 escherichia
31	15	22.4	13	2	Q6LCW4	Q6lcw4 pseudomonas

32	15	22.4	13	2	O9RFZ4	O9rfz4 mycoplasma
33	15	22.4	13	2	O88176	O88176 mus musculu
34	15	22.4	13	2	O9QW45	O9qw45 rattus sp.
35	15	22.4	13	2	Q9QY46	Q9qy46 mus sp. zip
36	14	20.9	13	1	BRK_PARID	P42717 parapolylbia
37	14	20.9	13	1	CRBL_VESMA	P17232 vespa manda
38	14	20.9	13	1	MP1_MICOC	P81532 microplitis
39	14	20.9	13	1	NP1_LYMT	P80178 lymnaea sca
40	14	20.9	13	1	NP2_LYMT	P80179 lymnaea sca
41	14	20.9	13	1	SODM_ARTDA	P83289 arthroboctry
42	14	20.9	13	1	SODM_CANFA	P54712 canis famil
43	14	20.9	13	1	TEM1_RANPI	P82848 rana pipien
44	14	20.9	13	1	TEM1_RANTE	P56918 rana tempor
45	14	20.9	13	1	YFE2_LACLC	P42021 lactococcus

ALIGNMENTS

RESULT 1
Q9UEE2 PRELIMINARY; PRT; 13 AA.
AC Q9UEE2;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
DE ERGB transcription factor (Fragment).
GN Name=FL11;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Obata K., Hiraga H., Nojima T., Yoshida M.C., Abe S.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB012625; BAA32806.1; -.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1541 MW; 2C67798CB566AB7 CRC64;

Query Match 32.8%; Score 22; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.7e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 QVSPYTL 11
| | | | |
DB 5 QPDYQIL 12
| | | | |

RESULT 2
IDHA_CANFA STANDARD; PRT; 13 AA.
AC P54836;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Isocitrate dehydrogenase (NAD) subunit alpha, mitochondrial
DE (EC 1.1.1.41) (isocitric dehydrogenase) (NAD+-specific IDH)
DE (Fragment).
GN Name=IDH3A;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
dog heart proteins.";
RL Electrophoresis 18:2795-2802 (1997).

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CC -|- CATALYTIC ACTIVITY: Isocitrate + NAD(+) = 2-oxoglutarate + CO(2) +
CC NADH.
CC -|- SUBUNIT: Heterooligomer of subunits alpha, beta, and gamma in the
CC apparent ratio of 2:1:1 (By similarity).
CC -|- SUBCELLULAR LOCATION: Mitochondrial.
CC -|- SIMILARITY: Belongs to the isocitrate and isopropylmalate
CC dehydrogenases family.
CC HSC-2DPAGE; P54936; DOG.
DR InterPro: IPR001804; Iscdh.
DR PROSITE: PS00470; IDH_IMDH; PARTIAL.
KW Direct protein sequencing; Mitochondrion; NAD; Oxidoreductase;
KW Tricarboxylic acid cycle.
FT NON TER 13
FT SEQUENCE 13 AA; 1356 MW; 9ABFBC2B2A34B2D1 CRC64;

Query Match 29.9%; Score 20; DB 1; Length 13;
Best Local Similarity 40.0%; Pred. No. 9.2e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 4 QVSPYTLKLG 13
Db 3 EVQTVTLIPG 12

RESULT 3
ID Q6T675 PRELIMINARY; PRT; 13 AA.
AC Q6T675;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE MHC class Ib antigen (Fragment).
GN Name=Paan-AG;
OS Papio anubis anubis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Papio.
OX NCBI_TaxID=211508;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=term placenta;
RA Langat D.K., Morales P.J., Fazleabas A.T., Hunt J.S.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AY34094; AAR12067.1; -.
FT NON TER 13
FT SEQUENCE 13 AA; 1456 MW; 3768BCEBF608B417 CRC64;

Query Match 29.9%; Score 20; DB 2; Length 13;
Best Local Similarity 57.1%; Pred. No. 9.2e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 5 VSPYTL 11
Db 4 MAPRTLL 10

RESULT 4
ID CHEP_PARID STANDARD; PRT; 13 AA.
AC P42718;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Chemotactic peptide.
OS Parapolybia indica.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Polistinae; Parapolybia.
OX NCBI_TaxID=31921;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Toki T., Yasuhara T., Nakajima T.;

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RT "Isolation and sequential analysis of peptides on the venom sac of
RT Parapolybia indica.";
RL Eisei Dobutau 39:105-111(1988).
KW Amidation; Chemotaxis; Direct protein sequencing.
FT MOD RES 13
FT SEQUENCE 13 AA; 1298 MW; 5C950CE8E39D5873 CRC64;

Query Match 28.4%; Score 19; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LLKG 13
Db 4 LLKG 7

RESULT 5
ID NF3_LYMST STANDARD; PRT; 13 AA.
AC P80180;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Lymnaea-DF-amide 3.
OS Lymnaea stagnalis (Great pond snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeidae; Lymnaeidae; Lymnaea.
OX NCBI_TaxID=6523;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RX MEDLINE=93238777; PubMed=8477756;
RA "Lymnaea stagnalis, a new family of neuropeptides from the pond snail,
RT "Lymnaea stagnalis. Clue to cholecystokinin immunoreactivity in
RT invertebrates?";
RL Eur. J. Biochem. 213:875-879(1993).
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- SIMILARITY: Related to the cholecystokinin (CKK) family.
DR PIR; S32473; S32473.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD RES 13
FT UNSURE 12
FT SEQUENCE 13 AA; 1462 MW; 9CA07BA3F5D58865 CRC64;

Query Match 28.4%; Score 19; DB 1; Length 13;
Best Local Similarity 42.9%; Pred. No. 1.4e+04;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 PYTLKLG 13
Db 1 PYDRISG 7

RESULT 6
ID Q14890 PRELIMINARY; PRT; 13 AA.
AC Q14890;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Mucin (Fragment).
GN Name=MUC5AC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Tracheobronchial mucosa;
RA Guyonnet-Duperat V., Audie J., Laine A., Buissine M.,
RA Zouitina-Gallieue S., Pigny P., Degand P., Porchet N.;
RT "Characterization of the human mucin gene MUC5AC: a consensus

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RT    cysteine-rich domain for 11p15 mucin genes.";
RL    Biochem. J. 0.0-0.0(1994);
DR    EMBL; Z34280; CAA84034.1; -.
FT    NON TER 1
SQ    SEQUENCE 13 AA; 1580 MW; 535DF5A5183B7767 CRC64;

Query Match      28.4%; Score 19; DB 2; Length 13;
Best Local Similarity 42.9%; Pred. No. 1.4e+04;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY    1 NOEQVSP 7
      : |||
      2 NKNQLPP 8

Db

RESULT 7
ID    Q51605 PRELIMINARY; PRT; 13 AA.
AC    Q51605;
DT    01-NOV-1996 (TREMBLrel. 01, Created)
DT    01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE    CeIE7 protein (Fragment).
GN    Name=ceIE7;
OS    Plasmid Cole7.
OC    other sequences; plasmids.
OX    NCBI_TaxID=2450;
RN    [1]
RP    SEQUENCE FROM N.A.
RX    MEDLINE=92293113; PubMed=1603061;
RA    Soong B.W.; Lu F.M.; Chak K.F.;
RT    "Characterization of the cea gene of the Cole7 plasmid.";
RL    Mol. Gen. Genet. 233:177-183(1992).
DR    EMBL; M62409; AAB98055.1; -.
DR    GO; GO:0015643; F:toxin binding; IEA.
DR    GO; GO:0030153; P:bacteriocin immunity; IEA.
DR    InterPro; IPR000290; Colicin_pyocin.
DR    Pfam; PF01320; Colicin_Pyocin; 1.
KW    Plasmid.
FT    NON TER 13
SQ    SEQUENCE 13 AA; 1501 MW; 9E75F892148CB045 CRC64;

Query Match      28.4%; Score 19; DB 2; Length 13;
Best Local Similarity 37.5%; Pred. No. 1.4e+04;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY    2 QEQVSPYT 9
      : |||
      4 KNSISDYT 11

Db

RESULT 8
ID    Q9RG00 PRELIMINARY; PRT; 13 AA.
AC    Q9RG00;
DT    01-MAY-2000 (TREMBLrel. 13, Created)
DT    01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE    Hypothetical protein (Fragment).
OS    Mycoplasma capricolum subsp. capricolum.
OC    Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX    NCBI_TaxID=40479;
RN    [1]
RP    SEQUENCE FROM N.A.
RX    STRAIN=8035;
RC    MEDLINE=20193983; PubMed=10727835; DOI=10.1016/S0378-1135(99)00204-7;
RA    Thiaucourt F., Lorenzon S., David A., Breard A.;
RT    "Phylogeny of the Mycoplasma mycoides cluster as shown by sequencing
of a putative membrane protein gene.";
RL    Vet. Microbiol. 72:251-268(2000).
DR    EMBL; AF162995; AAF15247.1; -.

KW    Hypothetical protein.
FT    NON TER 1
SQ    SEQUENCE 13 AA; 1459 MW; 0B63638AED35573B CRC64;

Query Match      28.4%; Score 19; DB 2; Length 13;
Best Local Similarity 42.9%; Pred. No. 1.4e+04;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY    6 SPYTLK 12
      : |||
      4 TPYLKK 10

Db

RESULT 9
ID    FRI2_PEA STANDARD; PRT; 13 AA.
AC    P83445;
DT    28-FEB-2003 (Rel. 41, Created)
DT    28-FEB-2003 (Rel. 41, Last sequence update)
DE    Ferritin 2, chloroplast (fragment).
OS    Pisum sativum (Garden pea).
OC    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC    eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
OX    NCBI_TaxID=3888;
RN    [1]
RP    SEQUENCE, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC    STRAIN=cv. Laxton's Progress; TISSUE=Leaf;
RA    Shingles R.; McCarty R.E.;
RL    Submitted (SEP-2002) to Swiss-Prot.
CC    -!- FUNCTION: Ferritin is an intracellular molecule that stores iron
in a soluble, nontoxic, readily available form. The functional
molecule, which is composed of 24 chains, is roughly spherical and
contains a central cavity into which the polymeric ferric iron
core is deposited.
CC    -!- SUBCELLULAR LOCATION: Chloroplast (inner envelope membrane), and
other plastids.
CC    -!- TISSUE SPECIFICITY: Leaves.
CC    -!- MISCELLANEOUS: On the 2D-gel the determined pI of this protein is:
4.74, its MW is: 25.7 kDa.
CC    -!- SIMILARITY: Belongs to the ferritin family.
DR    InterPro; IPR001519; Ferritin.
DR    ProSITE; PS00540; FERRITIN_1; PARTIAL.
DR    ProSITE; PS00204; FERRITIN_2; PARTIAL.
DR    ProSITE; PS09005; FERRITIN_LIKE; PARTIAL.
KW    Chloroplast; Direct protein sequencing; Iron; Iron storage;
Metal-binding.
FT    NON TER 13
SQ    SEQUENCE 13 AA; 1246 MW; 26C9DC25F334ADC7 CRC64;

Query Match      26.9%; Score 18; DB 1; Length 13;
Best Local Similarity 80.0%; Pred. No. 2.3e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY    6 SPYTL 10
      : |||
      5 SPATL 9

Db

RESULT 10
ID    NEUT_BUFMA STANDARD; PRT; 13 AA.
AC    P81756;
DT    16-OCT-2001 (Rel. 40, Created)
DT    16-OCT-2001 (Rel. 40, Last sequence update)
DE    Neurotensin (NT).
OS    Bufo marinus (Giant toad) (Cane toad).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Bufonidae; Bufo.
OX    NCBI_TaxID=8386;
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RN SEQUENCE, AND SYNTHESIS.
RP TISSUE=Small intestine.
RC MEDLINE=99000115; PubMed=9786176; DOI=10.1016/S0196-9781(98)00063-1;
RA Warner F.J., Burcher E., Carraway R., Conlon J.M.;
RT "Purification, characterization, and spasmogenic activity of
RL Neutroensin from the toad Bufo marinus.";
RL Peptides 19:1255-1261(1998).
CC -!- FUNCTION: Smooth muscle-contracting peptide. Peptide action is not
CC affected by tetrodotoxin, but is slightly mediated through the
CC release of acetylcholine.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the neurotensin family.
KW Direct protein sequencing; Pyrrolidone carboxylic acid; Vasoactive.
FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
SQ SEQUENCE 13 AA; 1515 MW; 56BD9F3A35410DD3 CRC64;

Query Match 25.4%; Score 17; DB 1; Length 13;
Best Local Similarity 75.0%; Pred. No. 3.5e+04;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 PYTL 10
Db 10 PYIL 13

RESULT 11
NEUT_CAVPO STANDARD; PRT; 13 AA.
AC P32560;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Neurotensin (NT).
GN Name=NTS;
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP TISSUE=Small intestine;
RC MEDLINE=86248085; PubMed=3087775; DOI=10.1016/0014-5793(86)80684-6;
RA Shaw C., Thim L., Conlon J.M.;
RT "[Ser7]neurotensin: isolation from guinea pig intestine.";
RL FEBS Lett. 202:187-192(1986).
CC -!- FUNCTION: Smooth muscle-contracting peptide.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the neurotensin family.
DR PIR; A53608;
KW Direct protein sequencing; Pyrrolidone carboxylic acid; Vasoactive.
FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
SQ SEQUENCE 13 AA; 1680 MW; 4C8314644C4115B3 CRC64;

Query Match 25.4%; Score 17; DB 1; Length 13;
Best Local Similarity 75.0%; Pred. No. 3.5e+04;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 PYTL 10
Db 10 PYIL 13

RESULT 12
NEUT_CHICK STANDARD; PRT; 13 AA.
AC P13724;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Neurotensin (NT).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE.
RX MEDLINE=88063566; PubMed=3682409;
RI Iwabuchi H., Komori S., Ohashi H., Kimura S.;
RT "The amino acid sequence of a smooth muscle-contracting peptide from
RL chicken rectum. Identity to chicken neurotensin.";
RL Jpn. J. Pharmacol. 44:455-459(1987).
CC -!- FUNCTION: Smooth muscle-contracting peptide.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the neurotensin family.
DR PIR; A28505;
KW Direct protein sequencing; Pyrrolidone carboxylic acid; Vasoactive.
FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
SQ SEQUENCE 13 AA; 1608 MW; 4C949E714C410DD3 CRC64;

Query Match 25.4%; Score 17; DB 1; Length 13;
Best Local Similarity 75.0%; Pred. No. 3.5e+04;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 PYTL 10
Db 10 PYIL 13

RESULT 13
NEUT_RANTE STANDARD; PRT; 13 AA.
AC P41536;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Neurotensin (NT).
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.
OX NCBI_TaxID=8407;
RN [1]
RP SEQUENCE.
RX MEDLINE=92245104; PubMed=1574601; DOI=10.1016/0167-0115(92)90069-7;
RA Shaw C., McKay D.M., Halton D.W., Thim L., Buchanan K.D.;
RT "Isolation and primary structure of an amphibian neurotensin.";
RL Regul. Pept. 38:23-31(1992).
CC -!- FUNCTION: Smooth muscle-contracting peptide.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Identified in brain, intestine, and rectum,
CC but not in stomach or skin.
CC -!- SIMILARITY: Belongs to the neurotensin family.
DR PIR; A61067; A61067.
KW Direct protein sequencing; Pyrrolidone carboxylic acid; Vasoactive.
FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
SQ SEQUENCE 13 AA; 1569 MW; 56A53D69EF410DD3 CRC64;

Query Match 25.4%; Score 17; DB 1; Length 13;
Best Local Similarity 75.0%; Pred. No. 3.5e+04;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 PYTL 10
Db 10 PYIL 13

RESULT 14
TY13_PHYRO STANDARD; PRT; 13 AA.
ID TY13_PHYRO
AC P04096;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tryptophyllin-13.
OS Phyllomedusa rohdei (Rohde's leaf frog).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
 OC Phyllomedusinae; Phyllomedusa.

OX NCBI_TaxID=8394;
 RN [1]
 RP SEQUENCE.
 RA Montecucchi P.C., Gozzini L., Erspamer V.;
 RT "Primary structure determination of a tryptophan-containing
 RT tridecapeptide from Phyllomedusa rohdei.";
 RL Int. J. Pept. Protein Res. 27:175-182 (1986).
 CC -|- SUBCELLULAR LOCATION: Secreted.
 CC -|- TISSUE SPECIFICITY: Skin.
 DR PIR: A05174; A05174.
 KW Amphibian defense peptide; Direct protein sequencing;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
 SQ SEQUENCE 13 AA; 1646 MW; 33BF33A212227773 CRC64;

Query Match 25.4%; Score 17; DB 1; Length 13;
 Best Local Similarity 60.0%; Pred. No. 3.5e+04;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 QVSPY 8
 Db 1 QEKPY 5

RESULT 15

Q6S4R5
 ID Q6S4R5 PRELIMINARY; PRT; 13 AA.
 AC Q6S4R5;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Alpha tubulin (Fragment).
 OS Leishmania chagasi
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=44271;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MHOM/BR/00/1669;
 RA Purdy J.E., Wilson M.E.;
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY466450; AAR89132.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 13 AA; 1488 MW; 3F361B0689741B18 CRC64;

Query Match 25.4%; Score 17; DB 2; Length 13;
 Best Local Similarity 42.9%; Pred. No. 3.5e+04;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 QEQVSPY 8
 Db 7 BEDVEEY 13

Search completed: April 12, 2005, 10:53:34
 Job time : 176 secs

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